

SEQUENCE LISTING

<110> SAKANO, SEIJI
ITO, AKIRA

<120> DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

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<140> 09/068,740

<141> 1998-06-18

<150> JP 7-299611

<151> 1995-11-17

<150> JP 7-311811

<151> 1995-11-30

<150> PCT/JP96/03356

<151> 1996-11-15

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro
50 55 60

Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp
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Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro
85 90 95

TOGETHER: E55555

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Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr
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Gln Arg His Leu Thr Val Gly Glu Glu Thr Ser Gln Asp Leu His Ser
130 135 140

Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu
145 150 155 160

His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp
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Pro Gly Trp Lys Gly Pro Tyr Cys
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35 40 45
Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro
50 55 60
Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp
65 70 75 80
Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro
85 90 95
Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp
100 105 110
Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr
115 120 125
Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser
130 135 140
Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu
145 150 155 160

His Tyr Tyr Gly	Glu Gly Cys Ser Val	Phe Cys Arg Pro Arg Asp Asp	165	170	175
Ala Phe Gly His	Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn		180	185	190
Pro Gly Trp Lys	Gly Pro Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly		195	200	205
Cys Asp Glu Gln His	Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys		210	215	220
Arg Val Gly Trp Gln	Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro		225	230	235
Gly Cys Leu His	Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln		245	250	255
Glu Gly Trp Gly	Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr		260	265	270
His His Lys Pro Cys	Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln		275	280	285
Gly Ser Tyr Thr Cys	Ser Cys Arg Pro Gly Tyr Thr Gly Ala Thr Cys		290	295	300
Glu Leu Gly Ile Asp	Glu Cys Asp Pro Ser Pro Cys Lys Asn Gly Gly		305	310	315
Ser Cys Thr Asp Leu	Glu Asn Ser Tyr Ser Cys Thr Cys Pro Pro Gly		325	330	335
Phe Tyr Gly Lys Ile	Cys Glu Leu Ser Ala Met Thr Cys Ala Asp Gly		340	345	350
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Glu	Gly	Trp	Gly 260	Gly	Leu	Phe	Cys	Asn 265	Gln	Asp	Leu	Asn	Tyr 270	Cys	Thr
His	His	Lys 275	Pro	Cys	Lys	Asn	Gly 280	Ala	Thr	Cys	Thr	Asn 285	Thr	Gly	Gln
Gly	Ser 290	Tyr	Thr	Cys	Ser	Cys 295	Arg	Pro	Gly	Tyr	Thr 300	Gly	Ala	Thr	Cys
Glu 305	Leu	Gly	Ile	Asp	Glu 310	Cys	Asp	Pro	Ser	Pro 315	Cys	Lys	Asn	Gly	Gly 320
Ser	Cys	Thr	Asp	Leu 325	Glu	Asn	Ser	Tyr	Ser 330	Cys	Thr	Cys	Pro	Pro 335	Gly
Phe	Tyr	Gly 340	Lys	Ile	Cys	Glu	Leu	Ser 345	Ala	Met	Thr	Cys	Ala 350	Asp	Gly
Pro	Cys	Phe 355	Asn	Gly	Gly	Arg	Cys 360	Ser	Asp	Ser	Pro	Asp 365	Gly	Gly	Tyr
Ser 370	Cys	Arg	Cys	Pro	Val	Gly 375	Tyr	Ser	Gly	Phe	Asn 380	Cys	Glu	Lys	Lys
Ile 385	Asp	Tyr	Cys	Ser	Ser 390	Ser	Pro	Cys	Ser	Asn 395	Gly	Ala	Lys	Cys	Val 400
Asp	Leu	Gly	Asp	Ala 405	Tyr	Leu	Cys	Arg	Cys 410	Gln	Ala	Gly	Phe	Ser 415	Gly
Arg	His	Cys 420	Asp	Asp	Asn	Val	Asp	Asp 425	Cys	Ala	Ser	Ser	Pro 430	Cys	Ala
Asn	Gly	Gly 435	Thr	Cys	Arg	Asp	Gly 440	Val	Asn	Asp	Phe	Ser 445	Cys	Thr	Cys
Pro 450	Pro	Gly	Tyr	Thr	Gly 455	Arg	Asn	Cys	Ser	Ala	Pro 460	Val	Ser	Arg	Cys
Glu 465	His	Ala	Pro	Cys	His 470	Asn	Gly	Ala	Thr	Cys 475	His	Glu	Arg	Gly	His 480
Arg	Tyr	Val	Cys	Glu 485	Cys	Ala	Arg	Gly	Tyr 490	Gly	Gly	Pro	Asn	Cys	Gln 495
Phe	Leu	Leu	Pro 500	Glu	Leu	Pro	Pro	Gly 505	Pro	Ala	Val	Val	Asp 510	Leu	Thr

Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
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Met Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly
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Arg Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu
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Lys Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly
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Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
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Ser Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala
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Trp Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn
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Asp Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly
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 Tyr Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe
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 Gly His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly
 180 185 190
 Trp Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser
 195 200 205
 Pro Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr
 210 215 220
 Gly Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys
 225 230 235 240
 Val His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn
 245 250 255
 Trp Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His
 260 265 270
 Gln Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys
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 Ala Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys
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 Lys Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr
 325 330 335
 Gly Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys
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 Ser His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val
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 Ala Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys
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 Pro Gly His Ser Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys
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 Ile Thr Met Gly Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp
 835 840 845
 Cys Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val
 850 855 860
 Trp Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys
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 900 905 910
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 915 920 925
 Asn Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr
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 Thr Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn
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 Val Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser
 965 970 975
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 980 985 990
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<212> PRT

<213> Homo sapiens

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 Arg Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu
 35 40 45
 Lys Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly
 50 55 60
 Ser Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala
 65 70 75 80
 Ser Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala
 85 90 95
 Trp Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn
 100 105 110
 Asp Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly
 115 120 125
 Met Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly
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 Val Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr
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 Trp Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser
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 Pro Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr
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 Gly Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys
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Gln	Ser	Gly	Gly	Lys	Phe	Thr	Cys	Asp	Cys	Asn	Lys	Gly	Phe	Thr	Gly
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 625 630 635 640
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 Ser Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr
 675 680 685
 Cys Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp
 690 695 700
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 Cys Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr
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 Gly Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro
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 850 855 860
 Trp Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys
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 885 890 895

0995593 11504

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Thr	Glu	His	Ile	Cys	Ser	Glu	Leu	Arg	Asn	Leu	Asn	Ile	Leu	Lys	Asn	945	950	955
Val	Ser	Ala	Glu	Tyr	Ser	Ile	Tyr	Ile	Ala	Cys	Glu	Pro	Ser	Pro	Ser	965	970	975
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Ala	Phe	Tyr	Trp	Cys	Leu	Arg	Lys	Arg	Arg	Lys	Pro	Gly	Ser	His	Thr	1060	1065	1070
His	Ser	Ala	Ser	Glu	Asp	Asn	Thr	Thr	Asn	Asn	Val	Arg	Glu	Gln	Leu	1075	1080	1085
Asn	Gln	Ile	Lys	Asn	Pro	Ile	Glu	Lys	His	Gly	Ala	Asn	Thr	Val	Pro	1090	1095	1100
Ile	Lys	Asp	Tyr	Glu	Asn	Lys	Asn	Ser	Lys	Met	Ser	Lys	Ile	Arg	Thr	1105	1110	1115
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Ala	Arg	Phe	Ala	Lys	Gln	Pro	Ala	Tyr	Thr	Leu	Val	Asp	Arg	Glu	Glu	1140	1145	1150
Lys	Pro	Pro	Asn	Gly	Thr	Pro	Thr	Lys	His	Pro	Asn	Trp	Thr	Asn	Lys	1155	1160	1165
Gln	Asp	Asn	Arg	Asp	Leu	Glu	Ser	Ala	Gln	Ser	Leu	Asn	Arg	Met	Glu	1170	1175	1180
Tyr	Ile	Val														1185		

<213> Homo sapiens

<223> Description of Combined DNA/RNA Molecule: cDNA to mRNA, and amino acid

 $\langle 222 \rangle$ (179) . . (2347)

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Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser	
145 150 155 160	
cag gac ctg cac agc agc ggc cgc acg gac ctc aag tac tcc tac cgc	706
Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg	
165 170 175	
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Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys	
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195 200 205	
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Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro	
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Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro	
225 230 235 240	
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245 250 255	
tgt atc cgc tat cca ggc tgt ctc cat ggc acc tgc cag cag ccc tgg	994
Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp	
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acc ttt aac aag gag atg atg tca cca ggt ctt act acg gag cac att Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr Glu His Ile 965 970 975	3345
tgc agt gaa ttg agg aat ttg aat att ttg aag aat gtt tcc gct gaa Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val Ser Ala Glu 980 985 990 995	3393
tat tca atc tac atc gct tgc gag cct tcc cct tca gcg aac aat gaa Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala Asn Asn Glu 1000 1005 1010	3441
ata cat gtg gcc att tct gct gaa gat ata cgg gat gat ggg aac ccg Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp Gly Asn Pro 1015 1020 1025	3489
atc aag gaa atc act gac aaa ata atc gat ctt gtt agt aaa cgt gat Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser Lys Arg Asp 1030 1035 1040	3537
gga aac agc tcg ctg att gct gcc gtt gca gaa gta aga gtt cag agg Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg Val Gln Arg 1045 1050 1055	3585
cgg cct ctg aag aac aga aca gat ttc ctt gtt ccc ttg ctg agc tct Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu Leu Ser Ser 1060 1065 1070 1075	3633
gtc tta act gtg gct tgg atc tgt tgc ttg gtg acg gcc ttc tac tgg Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp 1080 1085 1090	3681
tgc ctg cgg aag cgg cgg aag ccg ggc agc cac aca cac tca gcc tct Cys Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr His Ser Ala Ser 1095 1100 1105	3729
gag gac aac acc acc aac aac gtg cgg gag cag ctg aac cag atc aaa Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu Asn Gln Ile Lys 1110 1115 1120	3777
aac ccc att gag aaa cat ggg gcc aac acg gtc ccc atc aag gat tat Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile Lys Asp Tyr 1125 1130 1135	3825
gag aac aag aac tcc aaa atg tct aaa ata agg aca cac aat tct gaa Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His Asn Ser Glu 1140 1145 1150 1155	3873
gta gaa gag gac gac atg gac aaa cac cag cag aaa gcc cgg ttt gcc Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys Ala Arg Phe Ala 1160 1165 1170	3921

Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
165 170 175

Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr
 180 185 190
 Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly
 195 200 205
 His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp
 210 215 220
 Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro
 225 230 235 240
 Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly
 245 250 255
 Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val
 260 265 270
 His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp
 275 280 285
 Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln
 290 295 300
 Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr
 305 310 315 320
 Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala
 325 330 335
 Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys
 340 345 350
 Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly
 355 360 365
 Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser
 370 375 380
 His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys
 385 390 395 400
 Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys
 405 410 415
 Glu Ala Lys Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala
 420 425 430
 Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp
 435 440 445
 Ile Asn Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys
 450 455 460
 Arg Asp Leu Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala
 465 470 475 480

0995593 112901

Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys
 485 490 495
 Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu
 500 505 510
 Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr
 515 520 525
 Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala
 530 535 540
 Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys
 545 550 555 560
 Ser His Leu Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile Asp
 565 570 575
 Ser Cys Thr Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val Arg
 580 585 590
 Tyr Ile Ser Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser Gln
 595 600 605
 Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr
 610 615 620
 Tyr Cys His Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn
 625 630 635 640
 Gly Gly Thr Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser
 645 650 655
 Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser
 660 665 670
 Gln Asn Pro Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn Asp
 675 680 685
 Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His Ser
 690 695 700
 Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys
 705 710 715 720
 Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp Glu
 725 730 735
 Gly Thr Thr Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn Pro
 740 745 750
 Cys His Asn Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr Cys
 755 760 765
 Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr Asn
 770 775 780

Asp Cys Ser Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly
 785 790 795 800
 Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp
 805 810 815
 Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly
 820 825 830
 Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro
 835 840 845
 Gly His Ser Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys Ile
 850 855 860
 Thr Met Gly Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp Cys
 865 870 875 880
 Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val Trp
 885 890 895
 Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys Pro
 900 905 910
 Ser Gly Gln Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His
 915 920 925
 Pro Cys Thr Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val
 930 935 940
 Lys Thr Lys Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn
 945 950 955 960
 Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr
 965 970 975
 Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val
 980 985 990
 Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala
 995 1000 1005
 Asn Asn Glu Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp
 1010 1015 1020
 Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser
 1025 1030 1035 1040
 Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg
 1045 1050 1055
 Val Gln Arg Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu
 1060 1065 1070
 Leu Ser Ser Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala
 1075 1080 1085

099559 4 1990


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<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence
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<400> 14
tggcartgya aytgycarga                                20
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```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

```
<400> 15
atyttytyt crcarttraa                20
```

```
<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

```
<220>  
<221> modified_base  
<222> (12)  
<223> a, t, c, g, other or unknown
```

```
<400> 16
tgcststgyg anaccaactg                20
```

```
<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

20

<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

25

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<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

25

<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

28

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<223> Description of Artificial Sequence: Chemical
Synthesis

28

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<210> 22
<211> 55
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<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

36

```
<220>
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      Synthesis
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25

```
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28

<220>
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Synthesis

51

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<220>
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      Synthesis
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25

25

27

28

51

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 35

aaggatccgt tctgttggtc agaggccgcc t

31

<210> 36

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 36

cctctagacg cgtagagcgg ccgccaccgc ggtgga

36

<210> 37

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 37

ctatacgatg tactccattc ggtttaag

28

<210> 38

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 38

ggacgcgtct agagtcgacc tgcaggcatg c

31

<210> 39

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 39

ctatttatca tcatcatctt tataatctac gatgtactcc attcggttta ag

52

0099593-11901
T0621-E555550

<210> 40
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus

<220>
 <221> MOD_RES
 <222> (1)..(45)
 <223> "Xaa" represents a variable amino acid

<400> 40
 Xaa Xaa Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly
 20 25 30
 Xaa Xaa Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys
 35 40 45

<210> 41
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 41
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
 20 25 30
 Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys
 35 40 45

<210> 42
 <211> 45
 <212> PRT
 <213> Drosophila sp.

<400> 42
 Val Thr Cys Asp Leu Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly
 20 25 30
 Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp Tyr Cys
 35 40 45

<210> 43

<211> 45
 <212> PRT
 <213> *Xenopus laevis*

<400> 43
 Phe Val Cys Asp Glu Tyr Tyr Tyr Gly Glu Gly Cys Ser Asp Tyr Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ala Phe Gly His Phe Ser Cys Gly Glu Arg Gly
 20 25 30
 Glu Lys Leu Cys Asn Pro Gly Trp Lys Gly Leu Tyr Cys
 35 40 45

<210> 44
 <211> 45
 <212> PRT
 <213> *Gallus sp.*

<400> 44
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg Gly
 20 25 30
 Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Gln Tyr Cys
 35 40 45

<210> 45
 <211> 45
 <212> PRT
 <213> *Murine sp.*

<400> 45
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Asp Arg Gly
 20 25 30
 Glu Lys Met Cys Asp Pro Gly Trp Lys Gly Gln Tyr Cys
 35 40 45

<210> 46
 <211> 45
 <212> PRT
 <213> *Homo sapiens*

<400> 46
 Val Thr Cys Asp Asp Tyr Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
 1 5 10 15
 Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
 20 25 30

099559199
 T062T E655660


```

<400> 48
Val Thr Cys Asp Asp His Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
  1                    5                10                15

Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
      20                25                30

Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro Glu Cys
      35                40                45

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